AMENDMENTS TO THE CLAIMS

Please amend claims as follows:

1. **(Currently amended)** A method for identifying and/or quantifying a biological organism or a component thereof in a sample by detecting a nucleotide sequence characteristic of said biological organism, wherein said nucleotide sequence is homologous to at least 4 other nucleotide sequences from other biological organisms, comprising:

amplifying or copying said nucleotide sequences into target nucleotide sequences using primer pairs which are capable of amplifying or copying at least two of said target homologous nucleotide sequences from other organisms;

contacting ~~a target comprising the organism or components thereof with capture molecules~~ said amplified or copied nucleotide sequences with single-stranded different capture nucleotide sequences, at least two of said single-stranded nucleotide sequences specific of at least two of said target homologous nucleotide sequences being bound ~~to~~ in an array to an insoluble solid support, said array comprising at least four different bound single-stranded capture nucleotide sequences/cm^2 of solid support surface, and wherein said capture nucleotide sequences are able to specifically bind to a target nucleotide sequence without binding to said at least four homologous nucleotide sequences, and;

detecting specific hybridization of the target nucleotide sequence to said capture nucleotide sequences, ~~quantifying and/or recording a signal resulting from the specific binding between said targets and their corresponding specific capture molecules~~,

wherein said capture ~~molecules are~~ nucleotide sequence being bound to ~~an~~ the insoluble solid support ~~surface~~ at a specific location upon ~~an~~ the array, ~~said array having a density of at least 4 different bound capture molecules/cm^2 of solid support surface,~~ and

wherein the binding between said target nucleotide sequence ~~targets~~ and ~~their~~ its corresponding capture ~~molecules~~ nucleotide sequence forms a ~~said~~ signal at the expected location, ~~and~~ the detection of said signal allowing a ~~allows~~ discrimination of the ~~a~~ target nucleotide sequence being specific of said organism or ~~its~~ components of said organism from other ~~related~~ organisms or components of said organisms ~~other related components~~ from the same or other groups, sub-groups or sub-sub-groups of said organisms or components of said organisms.

2. **(Currently amended)** The method of claim 1, wherein said biological organism or said component of the biological organism is present in ~~a~~ the sample among at least 2 other ~~related~~ organisms or components of said other organisms.

3. **(Currently amended)** The method of claim 1, ~~wehrein~~ wherein said biological organism or said component of the biological organism is present in ~~a~~ the sample among at least 4 other ~~related~~ organisms or components of said other organisms.

4. **(Currently amended)** The method of claim 1, further comprising extracting ~~original~~ components from said organism.

5. **(Original)** The method of claim 1, further comprising labeling said organism or its components as targets.

6. **(Original)** The method of claim 1, wherein said organism is a microorganism.

7. **(Currently amended)** The method of claim 1, further comprising ~~the step of~~ identifying and/or quantifying the presence of several groups, sub-groups or sub-sub-groups of said organisms ~~components~~ or components of said organisms ~~comprising said components~~ being related to each other ~~until possible individual components or organisms,~~ wherein the binding between targets and corresponding specific capture molecules forms a signal at an expected location allowing the identification of a target specific of a group, sub-group or sub-sub-group of ~~components or~~ organisms comprising said components.

8. **(Currently amended)** The method of claim 7, wherein the array contains two categories of capture molecules, a first ~~one~~ category of capture molecules being specific for individual target components or their sub-groups and ~~the~~ a second ~~one~~ category of capture molecules being specific for all the components of the group.

9. **(Canceled)**

10. **(Currently amended)** The method of claim ~~9~~ 8, wherein the first category of capture molecules has a sequence length specific of the target of about 3 and about 60 bases and wherein the second category of capture nucleotide sequences has a sequence length specific of the target comprised between about 10 and about 1000 bases.

11. **(Original)** The method of claim 10, wherein said second category of capture nucleotide sequences has a sequence length specific of the target comprised between about 100 and 600 bases.

12. **(Currently amended)** The method of claim ~~9~~ 1, wherein the amplified target sequences are homologous polynucleotides and are discriminated on the array upon corresponding polynucleotide capture sequences.

13. **(Currently amended)** The method of claim ~~9~~ 1, wherein the amplified ~~original polynucleotide sequences are~~ nucleotide sequence is a DNA nucleotide sequences.

14. **(Currently amended)** The ~~identification~~ method of claim ~~9~~ 1, wherein all or most of the amplified sequences are obtained by PCR with the same primer pair.

15. **(Currently amended)** The method of claim ~~9~~ 1, wherein the presence of any amplified sequence is firstly detected during the genetic amplification cycles and thereafter identified on the array.

16. **(Currently amended)** The method of claim ~~9~~ 1, wherein the step of detecting the presence of any amplified sequences and the genetic amplification step are performed in a same chamber.

17. **(Currently amended)** The method of claim ~~9~~ 1, wherein the amplified nucleotide sequence is mRNA first ~~retrotranscribed~~ reverse transcribed into cDNA and then amplified with the same primer pair which is capable of amplifying at least two of said homologous mRNA is said sample.

18. **(Currently amended)** The method of claim ~~9~~ 1, wherein the nucleotide sequences are copied by using the same primer pair.

19. **(Currently amended)** The method of claim ~~9~~ 1, wherein the ~~specific sequence of the~~ single-stranded capture nucleotide sequence~~, able to hybridize with their corresponding target nucleotide sequence,~~ is ~~separated from the surface of~~ bound in an array to the solid support ~~by~~ via a spacer ~~having~~ which is at least 6.8 nm in length.

20. **(Original)** The method of claim 19, wherein said spacer is a nucleotide sequence of between about 15 and about 1000 bases.

21. **(Original)** The method of claim 19, wherein said spacer is a nucleotide sequence of between about 30 and about 120 bases.

22. **(Original)** The method of claim 19, wherein the spacer is a polymeric chain of at least 10 atoms, selected from the group consisting of poly-ethyleneglycol, polyaminoacids, polyacrylamides, poly-aminosaccharides, polyglucides, polyamides, polyacrylates, polycarbonates, polyepoxides, poly-ester and a mixture thereof.

23. **(Original)** The method of claim 19, wherein said polymeric chain is branched.

24. **(Currently amended)** The method of claim ~~9~~ 1, wherein the length of the specific sequence of the capture nucleotide sequence able to hybridize with the corresponding target nucleotide sequences is comprised between about 5 and about 60 bases.

25. **(Original)** The method of Claim 24, wherein the corresponding target nucleotide sequences is comprised between about 20 and about 30 bases.

26. **(Currently amended)** The method of claim ~~9~~ 1, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 10 fmoles per cm^2 of solid support surface.

27. **(Currently amended)** The method of claim ~~9~~ 1, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 100 fmoles per cm^2 of solid support surface.

28. **(Currently amended)** The method of claim ~~9~~ 1, wherein the capture nucleotide sequences bound to the solid support surface at a specific location are bound to the support by covalent binding.

29. **(Currently amended)** The method of claim ~~9~~ 1, wherein the capture nucleotide sequences bound to the solid support surface at a specific location are polynucleotides.

30. **(Currently amended)** The method of claim ~~9~~ 1, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 40% with other homologous nucleotide sequences.

31. **(Currently amended)** The method of claim ~~9~~ 1, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 60% with other homologous nucleotide sequences.

32. **(Currently amended)** The method of claim ~~9~~ 1, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 80% with other homologous nucleotide sequences.

33. **(Currently amended)** The method of claim ~~9~~ 1, wherein the target nucleotide sequences are labelled by a marker and wherein the signal resulting from hybridization by complementary bases pairing between the target nucleotide sequence and its corresponding capture nucleotide sequence is obtained from the detection of said marker.

34. **(Currently amended)** The method of claim ~~9~~ 1, wherein the target nucleotide sequences are cut into pieces before putting into contact with the single stranded capture nucleotide sequences bound to the solid support.

35. **(Currently amended)** The method of claim ~~9~~ 1, wherein other primers are present in the amplification step for the amplification of other nucleotide sequences, such as an antibiotic resistance determining sequence.

36. **(Currently amended)** The method of claim ~~9~~ 1, wherein the nucleotide sequences to be detected and/or be quantified are RNA sequences submitted to a retro-transcription of the 3' or 5' end by using a member selected from the group consisting of a consensus primer and a stopper sequence.

37. **(Currently amended)** The method of claim ~~9~~ 1, wherein the solid support surface comprises capture nucleotide sequences specific for the binding of homologous target nucleotide sequences together with a consensus sequence for a common detection.

38. **(Currently amended)** The method of claim ~~9~~ 1, wherein the solid support comprises capture nucleotide sequences specific for the identification of two or more staphylococcus species together with a consensus sequence for a *Staphylococcus* genus identification.

39. **(Currently amended)** The method of claim ~~9~~ 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample differs from at least one of its homologous sequences present in the sample by one or more base(s).

40. **(Currently amended)** The method of claim ~~9~~ 1, wherein the arrays contained two to four capture nucleotide sequences differing from each other by one or more base(s).

41. **(Original)** The method of claim 1, wherein the component to be detected and/or quantified is a protein and the capture molecule an antibody or an hypervariable portion thereof.

42. **(Original)** The method of claim 41, wherein the target is bound to the capture molecule by one of its epitopes.

43. **(Currently amended)** The method of claim 37, wherein the capture molecule ~~is~~ comprises a monoclonal antibody or an hypervariable portion thereof.

44. **(Original)** The method of claim 1, wherein the quantification of the organism present in the biological sample is obtained by the quantification of the signal.

45. **(Original)** The method of claim 1, wherein the insoluble solid support is selected from the group consisting of glass, an electronic device, a silicon support, a plastic support, silica, metal and a mixture thereof, wherein said support is prepared in a prepared in a format selected from the group consisting of slides, discs, gel layers and microbeads.

46. **(Currently amended)** The method of claim ~~1~~ 6, wherein the microorganism to be identified and/or quantified in the sample belongs to the Staphylococci species selected from the group consisting of *S. aureus, S. epidermidis, S. saprophyticus, S. hominis* and *S. haemolyticus*.

47. **(Currently amended)** The method of claim ~~1~~ 6, wherein the microorganism to be identified and/or quantified in the sample belong to the Mycobacteria genus.

48. **(Original)** The method of claim 1, wherein the component to be identified and/or quantified in the sample is a sequence which belongs to the MAGE family.

49. **(Original)** The method of claim 1, wherein the component to be identified and/or quantified in the sample is a sequence which belongs to the *HLA-A* family.

50. **(Currently amended)** The method of claim 1, wherein the component to be identified and/or quantified in the sample is a G protein-coupled receptor.

51. **(Currently amended)** The method of claim ~~49~~ 50, wherein the component to be identified and/or quantified in the sample is a dopamine receptor.

52. **(Currently amended)** The method of claim ~~49~~ 50, wherein the component to be identified and/or quantified in the sample is a choline receptor.

53. **(Currently amended)** The method of claim ~~49~~ 50, wherein the component to be identified and/or quantified in the sample is a histamine receptor.

54. **(Currently amended)** The method of claim 1, wherein the component to be identified and/or quantified in the sample is a sequence which belongs the Cytochrome P450 ~~forms~~ isoforms family.

55. **(Currently amended)** The method of claim ~~1~~ 6, wherein the microorganism to be identified and/or quantified in the sample belongs to ~~the~~ a Gram-positive or Gram-negative family bacteria.

56. **(Original)** The method of claim 7, wherein the group, sub-group or individual targets correspond to families, genus, species, subtypes or individual organisms.

57. **(Original)** The method of claim 7, wherein the families, genus, species, subtypes or individuals are bacteria.

58. **(Original)** The method of claim 57, wherein bacteria belonging to at least two of the genus families selected from the group consisting of *Staphylococcus*, *Enterococcus*, *Streptococcus*, *Haemolyticus*, *Pseudomonas*, *Campylobacter*, *Enterobacter*, *Neisseria*, *Proteus*, *Salmonella*, *Simonsiella*, *Riemerella*, *Escherichia*, *Neisseria*, *Meningococcus*, *Moraxella*, *Kingella*, *Chromobacterium* and *Branhamella*.

59. **(Currently amended)** The method of claim ~~9~~ 1, wherein the identification of the nucleotide sequences allows an identification of the polymorphism of an organism.

60. **(Currently amended)** The method of claim ~~9~~ 1, wherein the identification of the nucleotide sequences allows the genotyping of an organism.

61. **(Currently amended)** The method of claim ~~9~~ 1, wherein the identification of the nucleotide sequences allows the identification of a single nucleotide polymorphism.

62. - 79. **Canceled**

80. **(New)** The method of claim 1, wherein the capture nucleotide sequences comprise a nucleotide sequence of about 10 to about 60 bases, which is able to specifically bind to said target nucleotide sequence without binding to said at least four homologous nucleotide sequences.

81. **(New)** The method of claim 1, wherein said capture nucleotide sequences comprise a nucleotide sequence of between about 15 and about 40 bases, which is able to specifically bind to said target nucleotide sequence without binding to said at least four homologous nucleotide sequences from other organisms.

82. **(New)** The method of claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is more than 10 fmoles per cm^2 of solid support surface.

83. **(New)** The method of claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 30%.

84. **(New)** The method of claim 1, wherein other primers are present in the amplification step for the amplification of another nucleotide sequence.

85. **(New)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified is an RNA sequence submitted to a reverse transcription of its 3' or 5' end by using a consensus primer.

86. **(New)** The method of claim 1, wherein the nucleotide sequences to be identified and/or quantified are from the *FemA* gene of Staphylococci species selected from the group consisting of *S. aureus*, *S. epidermidis*, *S. saprophyticus*, *S. hominis* and *S. haemolyticus*.

87. **(New)** The method of claim 1, wherein the solid support also bears another capture consensus nucleotide sequence able to bind to said target nucleotide sequence and to said at least four homologous nucleotide sequences.

88. **(New)** The method of claim 2, wherein the spacer is a non-specific nucleotide sequence of at least 20 nucleotides.

89. **(New)** The method of claim 58, wherein the said gene is a gene encoding sub-unit A of gyrase.

90. **(New)** The method of claim 54, wherein the Cytochrome P450 isoforms family comprises a Cytochrome P450 2D6 and a 2C19 isoforms.

91. **(New)** The method of claim 1, wherein the sequences to be identified and/or quantified in the samples come from different animal species and genus belonging to families: *Galinaceae*, *Leporidae*, *Suidae* and *Bovidae*.

92. **(New)** The method of claim 1, wherein the sequences to be detected and/or quantified in the samples belong to specific fishes species selected from the group consisting of *G. morhua, G. macrocephalus, P. flesus, M. merluccius, O. mykiss, P. platessa, P. virens, S. salar, S. pilchardus, A. thazard, T. alalunga, T. obesus, R. hippoglossoides, S. trutta, S. sarda, T. thynnus, S. scombrus* belonging to genera selected from the group consisting of: as Auxis, Sarda, Scomber, Thunnus, Oncorhynch, Salmo, Merluccius, Pleuronectes, Platichtlys, Reinhardtius, Pollachius, Gadus, Sardina, from several families selected from the group consisting of: *Scombridae, Salmonidae, Merluccidae, Pleuronectidae, Gadidae* and *Clupeidae*.

93. **(New)** The method of claim 1, wherein the sequences to be detected and/or quantified in the samples belong to different plant species and genus such as Potato, tomato, oryza, zea, soja, wheat, barley, bean and carrot.

94. **(New)** The method of claim 1, wherein the sequences to be detected and/or quantified in the samples are genetically modified organisms.